AMENDMENT

Amendment to the Specification:

At page 1, line 3, please insert the following paragraph:

--This application is a national phase application under 35 U.S.C. § 371 of International Application No. PCT/EP2004/003398 filed 31 March 2004, which claims priority to European Application No. 03450078.5 filed 31 March 2003. The entire text of each of the above-referenced disclosures is specifically incorporated herein by reference without disclaimer.--

At page 3, please replace the last paragraph spanning pages 3-4, with the following substitute paragraph:

> Individuals undergoing ~~continous~~ continuous peritoneal dialysis represent one of the most important groups of patients infected by S. epidermidis. Staphylococci preferentially infect patients with foreign bodies such as dialysis catheters. Peritoneal dialysis patients suffer from peritonitis mainly caused by S. aureus and coagulase negative staphylococci, especially S. epidermidis. In order to identify antigens expressed by S. epidermidis in humans during peritonitis, human serum samples were collected from patients undergoing peritoneal dialysis for an extended period of time and suffered from peritonitis caused by S. epidermidis within the previous 12 months, and thus considered to be in the late convalescent phase of the disease. It has been firmly established that patients with serious staphylococcal diseases - such as peritonitis - develop antibodies, which sustain for up to a year.

At page 6, please replace the paragraph spanning pages 6-8 with the following substitute paragraph:

> According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa"

and "location of identified immunogenic region" of Table 1; the serum reactive epitopes of ~~Table 2~~ Table 1, especially peptides comprising amino acids 6-28, 54-59, 135-147, 193-205, 274-279, 284-291, 298-308, 342-347, 360-366, 380-386, 408-425, 437-446, 457-464, 467-477, 504-510, 517-530, 535-543, 547-553, 562-569, 573-579, 592-600, 602-613, 626-631, 638-668 and 396-449 of Seq ID No 32; 5-24, 101-108, 111-117, 128-142, 170-184, 205-211, 252-267, 308-316, 329-337, 345-353, 360-371, 375-389, 393-399, 413-419, 429-439, 446-456, 471-485, 495-507, 541-556, 582-588, 592-602, 607-617, 622-628, 630-640 and 8-21 of Seq ID No 33; 10-20, 23-33, 40-45, 59-65, 72-107, 113-119, 127-136, 151-161 and 33-59 of Seq ID No 34; 4-16, 28-34, 39-61, 66-79, 100-113, 120-127, 130-137, 142-148, 150-157, 192-201, 203-210, 228-239, 245-250, 256-266, 268-278, 288-294, 312-322, 336-344, 346-358, 388-396, 399-413, 425-430, 445-461, 464-470, 476-482, 486-492, 503-511, 520-527, 531-541, 551-558, 566-572, 609-625, 635-642, 650-656, 683-689, 691-705, 734-741, 750-767, 782-789, 802-808, 812-818, 837-844, 878-885, 907-917, 930-936 and 913-933 of Seq ID No 35; 5-12, 20-27, 46-78, 85-92, 104-112, 121-132, 150-167, 179-185, 200-213, 221-227, 240-264, 271-279, 282-290, 311-317 and 177-206 of Seq ID No 36; 18-24, 31-40, 45-51, 89-97, 100-123, 127-132, 139-153, 164-170, 184-194, 200-205, 215-238, 244-255, 257-270, 272-280, 289-302, 312-318, 338-348, 356-367 and 132-152 of Seq ID No 37; 7-16, 39-45, 73-83, 90-98, 118-124, 130-136, 194-204, 269-280, 320-327, 373-381, 389-397, 403-408, 424-430, 436-441, 463-476, 487-499, 507-514, 527-534, 540-550, 571-577, 593-599, 620-629, 641-647, 650-664, 697-703, 708-717, 729-742, 773-790, 794-805, 821-828, 830-837, 839-851, 858-908, 910-917, 938-947, 965-980, 1025-1033, 1050-1056, 1073-1081, 1084-1098, 1106-1120, 1132-1140, 1164-1170, 1185-1194, 1201-1208, 1215-1224, 1226-1234, 1267-1279, 1325-1331, 1356-1364, 1394-1411, 1426-1439, 1445-1461, 1498-1504, 1556-1561, 1564-1573, 1613-1639, 1648-1655, 1694-1714, 1748-1755, 1778-1785, 1808-1813, 1821-1827, 1829-1837, 1846-1852, 1859-1865, 1874-1883, 1895-1900, 1908-1913, 1931-1937, 1964-1981, 1995-2005, 2020-2033, 2040-2047, 2103-2109, 2118-2127, 2138-2144, 2166-2175, 2180-2187,

2220-2225, 2237-2242, 2247-2253, 2273-2281, 2286-2306, 2314-2320, 2323-2345, 2350-2355, 2371-2384, 2415-2424, 2426-2431, 2452-2472, 2584-2589, 2610-2621, 2638-2655, 2664-2670, 2681-2690, 2692-2714, 2724-2730 and 687-730 of Seq ID No 38; 10-40, 53-59, 79-85, 98-104, 117-122, 130-136, 144-158, 169-175, 180-185, 203-223, 232-237, 243-254, 295-301 and 254-292 of Seq ID No 39; 28-50, 67-85, 93-115, 120-134, 144-179, 240-249, 328-340, 354-360, 368-400, 402-417, 419-427, 429-445, 447-455, 463-468, 472-480, 485-500, 502-510, 512-534, 537-546, 553-558, 582-594, 619-637, 645-654, 690-709, 735-745, 749-756, 786-792, 275-316 and 378-401 of Seq ID No 40; 5-16, 21-30, 33-40, 52-74, 101-108, 116-122, 164-182, 185-219, 256-261, 273-279, 285-291, 297-304, 312-328, 331-338, 355-362, 364-371, 373-401, 411-423 and 191-208 of Seq ID No 41; 34-55, 67-74, 85-93, 105-115, 138-152, 161-171, 182-189, 197-205, 213-219, 232-239, 241-248, 250-263, 272-277, 288-299 and 216-231 of Seq ID No 42; 21-27, 32-37, 43-51, 67-74, 82-92, 94-100, 106-112, 140-149, 153-159, 164-182, 193-215, 222-227, 260-267, 308-322, 330-340, 378-387, 396-403, 417-432, 435-441, 448-465, 476-482, 488-498, 500-510 and 214-280 of Seq ID No 43; 4-21, 29-52, 80-87, 104-123, 126-133, 141-157, 182-189, 194-202, 214-220, 227-235, 242-252 and 33-108 of Seq ID No 44; 12-18, 20-27, 29-59, 64-72, 84-90, 96-103, 109-121, 125-155, 164-177, 179-186, 188-201, 216-227, 235-253, 259-274, 276-294, 296-310, 322-339, 341-348, 369-379, 398-403, 409-421 and 76-96 of Seq ID No 45; 4-15, 24-41, 71-80, 104-111, 113-119, 123-130, 139-149, 168-178, 187-200 and 4-45 of Seq ID No 46; 13-19, 32-37, 44-56 and 1-14 of Seq ID No 47; 6-11, 16-35, 75-81, 95-100, 126-139, 206-214, 225-233, 241-259, 268-276, 319-325, 339-360, 371-401, 435-441, 452-459, 462-472, 491-503, 505-516, 549-556, 567-580, 590-595, 612-622, 624-630, 642-648, 656-662, 687-693, 698-704, 706-712, 736-750, 768-777, 784-789, 812-818, 847-858, 894-900, 922-931, 938-949, 967-984, 986-992, 1027-1032, 1041-1054, 1082-1088, 1091-1097, 1119-1124, 1234-1240, 1250-1258, 1274-1289, 1299-1305, 1392-1398, 1400-1405, 1429-1442, 1460-1474, 1505-1514, 1531-1537, 1540-1552, 1558-1571, 1582-1587, 1616-1623, 1659-1666, 1671-1677, 1680-1686, 1698-1704, 1706-1712,

1768-1774, 1783-1797, 1814-1819, 1849-1855, 1870-1876, 1890-1897, 1947-1953, 1972-1980, 1999-2013, 2044-2051, 2068-2084, 2093-2099, 2122-2131, 2142-2147, 2156-2163, 2170-2179, 2214-2220, 2235-2245, 2271-2281, 2287-2293, 2308-2317, 2352-2362, 2373-2378, 2387-2407, 2442-2448, 2458-2474, 2507-2516, 2531-2537, 2540-2551, 2555-2561, 2586-2599, 2617-2627, 2644-2649, 2661-2675, 2685-2692, 2695-2707, 2733-2739, 2741-2747, 2774-2783, 2788-2795, 2860-2870, 2891-2903, 2938-2947, 2973-2980, 2993-2999, 3004-3030, 3046-3059, 3066-3077, 3082-3088, 3120-3132, 3144-3149, 3153-3169, 3200-3212, 3232-3256, 3276-3290, 3308-3322, 3330-3338, 3353-3360, 3363-3371, 3390-3408, 3431-3447, 3454-3484, 3503-3515, 3524-3541, 3543-3550, 3560-3567, 3586-3599, 3616-3621, 3642-3647, 3663-3679, 213-276, 579-621 and 1516-1559 of Seq ID No 48; 19-41, 43-49, 55-62, 67-74, 114-121, 130-140, 188-197, 208-217, 226-232, 265-287, 292-299, 301-319, 372-394, 400-410, 421-427 and 12-56 of Seq ID No 49; 6-12, 44-51, 53-60, 67-88, 91-100, 104-123, 137-142, 148-158, 161-168, 175-201, 204-210, 222-231, 239-253, 258-264, 272-282 and 60-138 of Seq ID No 50; 4-63, 69-104, 110-121, 124-131, 134-152, 161-187, 204-221, 223-237, 239-296, 298-310, 331-365, 380-405, 423-451, 470-552, 554-562, 574-581, 592-649, 651-658, 661-671, 673-707, 713-734, 741-748, 758-765, 773-790 and 509-528 of Seq ID No 51; 89-94, 102-115, 123-129, 181-188, 200-206, 211-235, 239-249, 267-281, 295-310, 316-321, 331-341, 344-359, 365-386, 409-422, 443-453, 495-506, 514-521, 539-547, 553-560, 563-570, 586-596, 621-626, 633-638, 651-657, 666-683, 697-705, 731-739, 761-768, 865-883 and 213-265 of Seq ID No 52; 5-20, 24-34, 37-43, 92-102, 134-139, 156-162, 184-191, 193-205, 207-213, 225-231, 241-247, 259-267, 269-286, 337-350, 365-372, 378-386, 399-413, 415-421, 447-457, 467-481 and 145-183 of Seq ID No 53; 12-19, 29-41, 43-57, 80-98, 106-141, 143-156, 172-183, 185-210, 214-220, 226-234, 278-287 and 237-287 of Seq ID No 54; 5-12, 32-48, 50-72, 75-81, 88-94 and 16-40 of Seq ID No 55; 4-21, 29-42, 48-62, 65-80, 95-101, 103-118, 122-130, 134-140, 143-152, 155-165, 182-192, 198-208, 232-247, 260-268, 318-348, 364-369, 380-391, 403-411, 413-424 and 208-230 of Seq ID No 56; 4-18, 65-75, 82-92, 123-140, 144-159, 166-172,

188-194 and 174-195 of Seq ID No 57; 7-20, 58-71, 94-101, 110-119, 199-209, 231-242, 247-254, 267-277, 282-290, 297-306, 313-319, 333-342, 344-369, 390-402, 414-431, 436-448, 462-471 and 310-350 of Seq ID No 58; 4-25, 37-44, 53-59, 72-78, 86-99, 119-128, 197-203, 209-218, 220-226, 233-244, 246-254, 264-271, 277-289, 407-430, 437-445, 464-472, 482-488, 503-509 and 308-331 of Seq ID No 59; 4-12, 14-43, 52-58 and 43-58 of Seq ID No 60; 4-14, 21-29, 35-49 and 38-50 of Seq ID No 61; 4-19, 31-37, 58-72, 94-108 and 1-72 of Seq ID No 62.

At page 8, please replace the last paragraph, spanning pages 8-9, with the following substitute paragraph:

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKL5KLK (SEQ ID NO:63), neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

At page 9, please replace the last paragraph with the following substitute paragraph:

Moreover, the present invention ~~provids~~ provides a method for producing an antibody according to the present invention, characterized by the following steps:

At page 18, please replace the last paragraph, spanning pages 18-19, with the following substitute paragraph:

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a

contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in ~~tables 1 and 2~~ table 1, especially the sequences of ~~table 2~~ table 1 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published Staphylococcus epidermidis strain RP62A genome (http://www.tigr.org/tdb/mdb/mdbinprogress.html) and/or any other published S. epidermidis genome sequence or parts thereof. Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode for polypeptides having at least 1, preferably at least 2, preferably at least three different amino acid residues compared to the published S. epidermidis counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

At page 24, please replace the third paragraph with the following substitute paragraph:

The different polypeptides described herein can have therapeutic and/or diagnostic utilities. The present application identifies different ~~imunogenic~~ immunogenic polypeptides, and immunogenic polypeptide regions, characteristic of S.epi. An immunogenic polypeptide region can be present by itself or part of a longer length polypeptide. The polypeptides and polypeptide regions can be used in diagnostic applications to provide an indication as to whether a person is, or has been, infected with S. epi. For example, a polypeptide containing an S. epi immunogenic region can be used to generate S. epi antibodies, which can be used to detect

the presence of S. epi in serum; and a polypeptide containing an S. epi immunogenic region can be used to detect the presence of S. epi. antibodies in serum.

At page 28, please replace the last paragraph, spanning pages 28-31, with the following substitute paragraph:

Preferred examples of such fragments of a hyperimmune serum-reactive antigen are selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa", and "Location of identified immunogenic region" of Table 1; the serum reactive epitopes of ~~Table 2~~ Table 1, especially peptides comprising amino acid 6-28, 54-59, 135-147, 193-205, 274-279, 284-291, 298-308, 342-347, 360-366, 380-386, 408-425, 437-446, 457-464, 467-477, 504-510, 517-530, 535-543, 547-553, 562-569, 573-579, 592-600, 602-613, 626-631, 638-668 and 396-449 of Seq ID No 32; 5-24, 101-108, 111-117, 128-142, 170-184, 205-211, 252-267, 308-316, 329-337, 345-353, 360-371, 375-389, 393-399, 413-419, 429-439, 446-456, 471-485, 495-507, 541-556, 582-588, 592-602, 607-617, 622-628, 630-640 and 8-21 of Seq ID No 33; 10-20, 23-33, 40-45, 59-65, 72-107, 113-119, 127-136, 151-161 and 33-59 of Seq ID No 34; 4-16, 28-34, 39-61, 66-79, 100-113, 120-127, 130-137, 142-148, 150-157, 192-201, 203-210, 228-239, 245-250, 256-266, 268-278, 288-294, 312-322, 336-344, 346-358, 388-396, 399-413, 425-430, 445-461, 464-470, 476-482, 486-492, 503-511, 520-527, 531-541, 551-558, 566-572, 609-625, 635-642, 650-656, 683-689, 691-705, 734-741, 750-767, 782-789, 802-808, 812-818, 837-844, 878-885, 907-917, 930-936 and 913-933 of Seq ID No 35; 5-12, 20-27, 46-78, 85-92, 104-112, 121-132, 150-167, 179-185, 200-213, 221-227, 240-264, 271-279, 282-290, 311-317 and 177-206 of Seq ID No 36; 18-24, 31-40, 45-51, 89-97, 100-123, 127-132, 139-153, 164-170, 184-194, 200-205, 215-238, 244-255, 257-270, 272-280, 289-302, 312-318, 338-348, 356-367 and 132-152 of Seq ID No 37; 7-16, 39-45, 73-83, 90-98, 118-124, 130-136, 194-204, 269-280, 320-327, 373-381, 389-397, 403-408, 424-430, 436-441, 463-476, 487-499, 507-514, 527-534, 540-550, 571-577, 593-599, 620-629, 641-647, 650-

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At page 41, please replace the last paragraph, spanning pages 41-42, with the following substitute paragraph:

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5′□3′-linked nucleotides. Rather the oligonucleotides have two types of nucleotides: 2′-deoxyphosphorothioate, which activate RNase H, and 2′-modified nucleotides, which do not. The linkages between the 2′-modified nucleotides can be phosphodiesters, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating region, which contains between 3 and 5 2′-

deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2´- deoxyphosphorothioate nucleotides to activate ~~eucaryotic~~ eukaryotic and, particularly, mammalian RNase H. Protection from degradation is accomplished by making the 5´ and 3´ terminal bases highly nuclease resistant and, optionally, by placing a 3´ terminal blocking group.

At page 44, please replace the second paragraph with the following substitute paragraph:

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or ~~tramsdermal~~ transdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

At page 45, please replace the last paragraph, spanning pages 45-46, with the following substitute paragraph:

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic ~~polyppetides~~ polypeptides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

At page 46, please replace the last paragraph, spanning pages 46-47, with the following substitute paragraph:

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide, which has the amino acid sequence ~~NH_2-RLAGLLRKGGEKIGEKLKKIGQKIKNFFQKLVPQPE-COOH~~ NH_2-RLAGLLRKGGEKIGEKLKKIGQKIKNFFQKLVPQPE-COOH (SEQ ID NO:64). Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20

amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids, which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further ~~immunactivating~~ immunoactivating substances.

At page 47, please replace the second full paragraph with the following substitute paragraph:

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. ~~Preferablly~~ Preferably, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

At page 51, please replace the first full paragraph with the following substitute paragraph:

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its

~~acitivity~~ activity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

At page 54, please replace the last paragraph, spanning pages 54-55, with the following substitute paragraph:

A, LSE-70 library in lamB with P15-IgG (804), B, LSE-150 library in fhuA with P15-IgG (826), C, LSA-300 library in fhuA with P15-IgG (729), *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC {Kolaskar, A. et al., 1990}. §, ~~Fourty-two~~ Forty-two coagulase negative Staphylococcus or S. epidermidis strains were tested by PCR with oligonucleotides specific for the genes encoding relevant antigens. Since 6 of the 31 CNS strains were negative for all genes analysed, we eliminated these data from the summary, because these strains are most likely not closely related to S. epidermidis.

At page 60, please replace the first paragraph with the following substitute paragraph:

Libraries for frame selection. Two libraries (LSE-70 and LSE-150) were generated in the pMAL4.31 vector with sizes of approximately 70, 150 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 μg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic S. epidermidis DNA yielded 4x 105 to 2x 106 clones after frame selection. To assess the randomness of the libraries, approximately 600 randomly chosen clones of LSE-70 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown that 90% of the clones fell in the size range between 16 and 61 bp with an average size of 34 bp (Figure 2). ~~Allmost~~ Almost all sequences followed the 3n+1 rule, showing that all clones were properly frame selected.

At page 63, please replace the last paragraph, spanning pages 63-64, with the following substitute paragraph:

~~Examplarily~~ Exemplarily, a number of genes encoding immunogenic proteins were tested by PCR for their presence in 42 different coagulase negative Staphylococcus (CNS) or S. epidermidis strains. Figure 4 shows the PCR reaction for ORF1163 with all indicated 42 strains. It was expected that not all of the CNS strains represent S. epidermidis isolates. Therefore it was not surprising that 6 of the 31 CNS strains were negative for all genes ~~analysed~~ analyzed. Some of the eight selected genes encoding identified antigens and analysed by PCR, were present in many strains tested (e.g. ORF0026, ORF0217 and ORF1163), ~~redendering~~ rendering them as good candidates for further development. A few genes were present in only a smaller number of the tested 42 strains (e.g. ORF0742 and ORF2700). This result may indicate the absence of the gene in the analysed isolates, or it could be due to a variation in the sequence used for the oligonucleotide for the PCR analysis. Interestingly, none of the eight analysed genes showed any variation in size. Sequencing of the generated PCR fragment from one strain and subsequent comparison to the RP62A strain confirmed the amplification of the correct DNA fragment. Importantly, the identified antigens, which are well conserved in all strains in sequence and size constitute novel vaccine candidates to prevent infections by S. epidermidis. As can be seen in Table 1, 20 of the listed 30 S. epidermidis antigens have a homolog in S. aureus COL with at least 50% sequence identity at the amino acid level, 4 have homologs with an identity below 50% and 6 antigens do not possess a homologous sequence in S. aureus COL. This indicates that several of the antigens have also the potential to show cross-protection with other Staphylococcal strains such as S. aureus.

Please replace the Sequence Listing numbered pages 1-114, with the substitute Sequence Listing numbered pages 1-116 submitted herewith as Appendix A.